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Attorney's Docket No.: 16380-003001 / 2001-2425/2

1631

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : John R. Desjarlais
Serial No. : 10/071,859
Filed : February 6, 2002
Title : APPARATUS AND METHOD FOR DESIGNING PROTEINS AND PROTEIN LIBRARIES

Art Unit : 1631
Examiner : Marjorie A. Moran

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

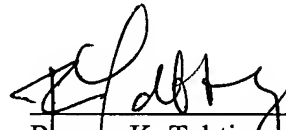
INFORMATION DISCLOSURE STATEMENT

Applicant submits the references listed on the attached form PTO-1449.

This statement is being filed within three months of the filing date of the application or before the receipt of a first Office action on the merits. Please apply any charges or credits to Deposit Account No. 06-1050, referencing docket number 16380-003001.

Respectfully submitted,

Date: Dec 30, 2003


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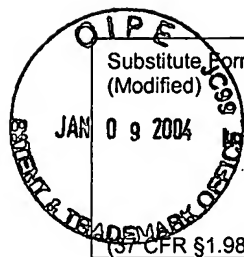
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Substitute Form PTO-1449
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Patent and Trademark OfficeAttorney's Docket No.
16380-003001Application No.
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(37 CFR §1.98(b))

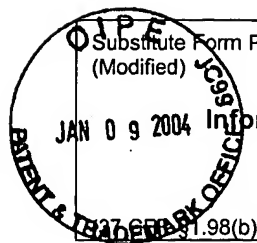
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1631**Other Documents (include Author, Title, Date, and Place of Publication)**

Examiner Initial	Desig. ID	Document
	AA	Dahiyat et al. "Automated design of the surface positions of protein helices." <i>Protein Science</i> . (1997), 6: 1333-1337.
	AB	Dahiyat et al. "Protein design automation." <i>Protein Science</i> . (1996), 5: 895-903.
	AC	Dahiyat et al. "De novo protein design: Fully automated sequence selection." <i>Science</i> . Vol. 278, 3 Oct. 1997, 82-87.
	AD	Dahiyat et al. "Probing the role of packing specificity in protein design." <i>Proc. Natl. Acad. Sci. USA</i> . Vol. 94, 10172-10177. Scot. 1997.
	AE	Dahiyat et al. "De novo protein design: Towards fully automated sequence selection." <i>J. Mol. Biol.</i> (1997)273, 789-796.
	AF	Delarue et al. "The inverse protein folding problem: Self consistent mean field optimisation of a structure specific mutation matrix." <i>Pac Symp Biocomput.</i> (1997), 109-121
	AG	Desjarlais et al. "Computer Search Algorithms in protein modification and design." (1998) <i>Curr Opin Struct Biol.</i> 8(4), 471-5.
	AH	Desjarlais et al. "De novo design of the hydrophobic cores of proteins." <i>Protein Science</i> (1995), 4,2006-18.
	AI	Desjarlais et al. "Side-chain and backbone flexibility in protein core design." <i>J. Mol. Biol.</i> (1999), 290(1), 305-18.
	AJ	Desmet et al., "The dead-end elimination theorem and its use in protein side-chain positioning." <i>Nature</i> . (1992), 356(9). 539-542.
	AK	Dunbrack et al. "Bayesian statistical analysis of protein side-chain rotamer preferences." <i>Protein Sci.</i> (1997) 6(8), 1661-81.
	AL	Eisenberg et al., "Solvation energy in protein folding and binding." <i>Nature</i> . 319(6050), 199-203.
	AM	Goldstein . "Efficient rotamer elimination applied to protein side-chains and related spin glasses." <i>Biophys. J.</i> (1994) 66(5), 1335-40.
	AN	Gordon. "Energy functions for protein design." <i>Curr Opin Struct Biol.</i> (1999), 9(4), 509-13.
	AO	Harbury et al. "Repacking protein cores with backbone freedom: structure prediction for coiled coils." <i>Proc Natl Acad Sci USA</i> . (1995), 92(18), 8408-12.
	AP	Hellinga. "Rational protein design: combining theory and experiment." <i>Proc Natl Acad Sci USA</i> . (1997), 94(19), 10015-17.

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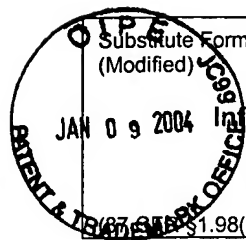
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1631**Other Documents (include Author, Title, Date, and Place of Publication)**

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	AQ	Hellinga et al. "Optimal sequence selection in proteins of known structure by simulated evolution." <i>Proc Natl Acad Sci USA</i> . (1994), 91(13), 5803-7.
	AR	Hendsch et al. "Electrostatic interactions in the GCN4 leucine zipper: Substantial contributions arise from intramolecular interactions enhanced on binding." <i>Protein. Sci.</i> (1999)8(7), 1381-92.
	AS	Henikoff et al. "Position-based sequence weights." <i>J. Mol. Biol.</i> (1994) 243(4), 574-8.
	AT	Holland. "Adaptation in natural and artificial systems." <i>The MIT Press</i> , Cambridge, MA (1992).
	AU	Johnson et al. "Solution structure and dynamics of a designed hydrophobic core variant of ubiquitin." <i>Structure Fold Des.</i> (1999), 7(8), 967-76.
	AV	Jorgensen et al. "The OPLS potential functions for proteins. Energy minimizations for crystals of cyclic peptides and crambin." <i>J. Amer. Chem. Soc.</i> (1988), 110(6), 1657-1666.
	AW	Koehl et al. "Application of a self-consistent mean field theory to predict protein side-chains conformation and estimate their conformational entropy." <i>J. Mol. Biol.</i> , 239(2), 249-75.
	AX	Koehl et al. "Mean-field minimization methods for biological macromolecules." <i>Curr Opin Struct Biol.</i> , (1996), 6(2), 222-6.
	AY	Kono et al. "Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry." <i>Proteins.</i> (1994), 19(3), 244-255.
	AZ	Kono et al. "Designing the hydrophobic core of <i>Thermus flavus</i> malate dehydrogenase based on side-chain packing." <i>Protein Eng.</i> (1998), 11(1), 47-52.
	AAA	Kuhlman et al. "Native protein sequences are close to optimal for their structures." <i>Proc. Natl. Acad. Sci. USA</i> . (2000), 97(19), 10383-8.
	ABB	Lazar et al. "De novo design of the hydrophobic core of ubiquitin." <i>Protein Sci.</i> (1997), 6(6), 1167-78.
	ACC	Lazar et al. "Rotamer strain as a determinant of protein structural specificity." <i>Protein Sci.</i> (1999), 8(12), 2598-610.
	ADD	Lee. "Predicting protein mutant energetics by self-consistent ensemble optimization." <i>J. Mol. Biol.</i> (1994), 236(3), 918-39.
	AEE	Micheletti et al. "Design of proteins with hydrophobic and polar amino acids." <i>Proteins.</i> (1998), 32(1), 80-7.
	AFF	Raha et al. "Prediction of amino acid sequence from structure." <i>Protein Sci.</i> (2000), 9(6), 1106-19.

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	AGG	Ranganathan et al. "Structural and functional analysis of the mitotic rotamase Pin1 suggests substrate recognition is phosphorylation dependent." <i>Cell</i> . (1997), 89(6), 875-86.
	AHH	Street et al. "Computational protein design." <i>Structure Fold Des.</i> (1999), 7(5), R105-9.
	AII	Su et al. "Coupling backbone flexibility and amino acid sequence selection in protein design." <i>Protein Sci.</i> (1997), 6(8), 1701-7.
	AJJ	Voigt et al. "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design." <i>J. Mol. Biol.</i> (2000), 299(3), 789-803.
	AKK	Voigt et al. "Computational method to reduce the search space for directed protein evolution." <i>Proc. Natl. Acad. Sci. USA.</i> (2001), 98(7), 3778-83.
	ALL	Weiner et al. "A new force field for molecular mechanical simulation of nucleic acids and proteins." <i>Journal of the American Chemical Society.</i> (1984). 106(3). 765-84.

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